3. Ze Fa EA EA

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Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-FN0143-190 700-022-d12&t3=2000-07-19&t4=1)
                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 564)
Dias Neto.E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Bala, G.S., Simpson, D.H., Marai, M.A., de Silva, W. Jr., Zago, M.A., Bordin, S., Simpson, D.H., Melani, A., deoliveire, P.S., Matsukuma, A., Bala, G.S., Simpson, D.H., M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                   BE839427 564 bp mRNA EST 22-SEP-2000
RC3-FN0143-190700-022-d12 FN0143 Homo sapiens cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shorgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
                                                                                                                                 BE839427.1 GI:10271805
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rel: +55-11-2704922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Simpson, A.J.
seq_documentation_block:
                                                                                                                                                                                                                                       Homo sapiens
                                                    DECESSION
VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                   ORGANISM
                                                                                                                                                                                                                                                                                                                                     REFERENCE
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seq primer: puc 18 forward
High quality sequence start: 18
High quality sequence start: 18
High quality sequence stop: 564.

Location/Qualifiers
1. 564

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108 a 156 c 121 g 179 t

BASE TO ORIGIN

alignment_scores:

Quality: 883.00 Length: 175 Ratio: 5.075 Gaps: 0 Percent Similarity: 99.429 Percent Identity: 98.857

alignment_block: US-09-513-365A-1 x BE839427/rev Align seg 1/1 to reverse of: BE839427 from: 1 to: 564

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1. .538
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Location/Qualifiers

source

FEATURES

Seq primer: M13 Forward

Enail: msoares@blue.weeg.uiowa.edu cDNA Library Preparation: M.B. Soares Lab Clone distribution: clones will be available through Research Genetics (www.resgen.com) This clone is also available through the I.M.A.G.E. Consortium at LLNL (info@image_llnl.gov). IMAGE ID- 1792594 Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Bonaldo,M.F., Lennon,G. and Soares,M.B. Normalization and subtraction: two approaches to facilitate gene University of Iowa 451 Eckstein Medical Research Building Iowa City, IA 52242, USA 11-DEC-2000 BF523624 538 bp mRNA EST 11-DEC-2000 UI-R-C1-lc-d-10-0-UI.rl UI-R-C1 Rattus norvegicus cDNA clone UI-R-C1-lc-d-10-0-UI 5', mRNA sequence. 284 AGCTTCTCCAGAGAGCACTAATTAATAGTCAAGAATTGGGAGATGAAAAA 235 101 IleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArgG1 117 nMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluArgA 134 134 laSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerArg 150 151 ArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMetAl 167 84 InLeuLeuGlnArgAlaLeuIleAsnSerGlnGluLeuGlyAspGluLys 100 234 ATACAGATTGTTACACAAATGCTCGAATTGGTGGAAAATCGGGCAAGACA 185 84 AGACCCCGCAGGCAGCGGACCAGTGTAAAGCCGTGATTTATGTCACATGGC 35 84 rGluLysTyrLysLysGluAspAspLeuAsnGlnLysLysArgLeuGlnG GluLeuAspAsnLysTyrGlnGluThrLeuLysGluIleAspAspValTy Contact: Soares, MB Program for Rat Gene Discovery and Mapping Genome_Res. 6 (9), 791-806 (1996) 167 aAsnGlyIleGluAspCysAspAsp 175 34 AAATGGGATTGAAGACTGTGATGAG 10 BF523624.1 GI:11631591 538 bp (bases 1 to 538) Tel: 319 335 8250 Fax: 319 335 9565 norvegicus seq_name: gb_est89:BF523624 seq_documentation_block: Norway rat. discovery BF523624 97044477 Rattus Rattus. EST KEYWORDS SOURCE ORGANISM DEFINITION ACCESSION AUTHORS MEDLINE REFERENCE JOURNAL 21 67 117 TITLE VERSION

87

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150 rgArgProArgArgGlnArgThrSerGluSerArgAspLeuCysHisMet 166
                                                                                                                                                                        167 AlaAsnGlyIleGluAspCysAspAspGlnProProLysGluLysLysSe 183
186 GGCCTCAGACAATCCAAGATGGATTCCAGTCAACCCGAAAGATCTTCCA 137
                                                                                                                                                                                                    183 rLysSerAlaLysLysLysArg 191
                                                                                                                                                                                                                                                                                                                               36 CAAATCCGCCAAAAAAAAAAAA 12
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COMMENT
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VERSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 ysIleGlnIleValThrGlnMetLeuGluLeuValGluAsnArgAlaArg 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 GlnMetGluLeuHisSerGlnCysPheGlnAspProAlaGluSerGluAr 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           386 TATGAAAATATAAGAAGAAGATGATTCAAACCAGAAAAAACGCCTACA 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      133 gAlaSerAspLysAlaLysMetAspSerSerGlnProGluArgSerSerA 150
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rgGluLeuAspAsnLysTyrGlnGluThrLeuLysGluIleAspAspVal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 175
Gaps: 0:
Percent Identity: 96.571
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ORIGIN
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/ Site_2: Smal; A mini-library was made by cloning
products derived from ORESTES PCR (U.S. Letters Patent
application No. 196,716 - Ludwig Institute for Cancer
Research) profiles into the puc 18 vector. Reverse
transcription of tissue mRNA and cDNA amplification were
performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=&t2=RC3-FN0143-260.00.012-c12&t3=R000-00-26&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence start: 21
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                 Dias Neto, E., Garcia Correa, R., Verjovski-Almelda, S., Briones, M.R., Nagal, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F., Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H., Brunstein, A., deoliveir, P.S., Bucher, P., Jongeneel, C.V., O'Hare, M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J. and
                                           Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
                                                                                                                                                                                                                                                                                Chordata; Craniata; Vertebrata; Eutele
Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
20202663
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Gaps: 0
Percent Identity: 98.817
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
                                                                                                                                                                  BE839460.1 GI:10271838
                                                                                                                                                                                                                                                         Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Ratio: 5.041
Percent Similarity: 100.000
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AY007790 Homo sapiens p47
AK000096 Homo sapiens cDNA
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                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (07-APR-1998) to the DDBJ/EMBL/GenBank databases.
Submitted (07-APR-1998) to the DDBJ/EMBL/GenBank databases.
Yoshikazu Shimada, Otsuka Pharmaceutical Co. Ltd., Otsuka GEN
Research Institute; Kagasuno, Kawauchi-cho, Tokushima, Tokushima
771-0192, Japan (E-mail:shim@ctsuka.genome.ad.jp,
Tel:81-886-65-2888(ex.2476), Fax:81-886-37-1035)
Sequence updated (17-Apr-1998).
I. 1078
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                                                                                                                                                                                                                                                                                                                                                                  Shimada,Y, Saito,A, Suzuki,M, Takahashi,E. and Horie,M. Cloning of a novel gene (ING1L) homologous to ING1, a candidate
                                                                                                                                                                                                                                                                  Homo sapiens fetal tissue_lib:fetal-brain cDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            92 ATGTTAGGGCAGCAGCAGCAGCAACTGTACTCGTCGGCCGCGCTCGAC 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 MetLeuGlyGlnGlnGlnGlnGlnLeuTyrSerSerAlaAlaLeuLeuTh 17
                                                                                                                                                   AB012853 1078 bp mRNA PRI HOMO Sapiens ING1L mRNA for ING1Lp, complete cds. AB012853 GI:4115554
                                                                                                                                                                                                                                                                                                                                                                                                                              Cytogenet. Cell Genet. 83 (3-4), 232-235 (1998) 99172097
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    1819
1839
2317
1982
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  8.7e-18
8.8e-18
1.2e-17
6.7e-17
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Shimada,Y., Saito,A. and Horie,M.
Direct Submission
  467.22
467.12
465.03
451.32
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92. .93
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  359.00
359.00
359.00
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Ratio: .5.289
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                   tumor suppressor
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US-09-513-365A-1 x AB012853
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                                                                                                                                            seq_documentation_block:
LOCUS AB012853
                                                                                                                                                                                                                                                                                         Homo sapiens
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Shimada,Y.,
                                                                                                                                                                                                                                               ING1Lp.
  gb_pr7:AY007790
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gb_pat2:AX078253
gb_ro1:AY007791
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AUTHORS
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TITLE
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AF181850 Homo sapiens ING1 tun
AF181850 Homo sapiens BRNA for
AF181850 Homo sapiens P331NG11
AF17755 Mus musculus ING1 prc
AF177755 Mus musculus ING1 prc
AF177755 Homo sapiens ING1 tun
AF149722 Homo sapiens ING1 tun
AR079046 Sequence 1 from paten
AR087467 Sequence 1 from paten
AR087464 Sequence 9 from paten
AR0875 Sequence 9 from paten
AR0875 Sequence 9 from paten
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2891 AB024402 Homo sapiens mRNA for 12925 AB037387 Homo sapiens ING1 gen 159983 AL157820 Homo sapiens clone 165376 AL157820 Homo sapiens chromos 86703 AL159899 Homo sapiens chromos IL0000 Continuation (4 of 6) of HSX 1377 AR10645 Homo sapiens candidate 1367 AR063594 Homo sapiens candidate 1367 AR063594 Homo sapiens, Similar MY 618 BC005370 Homo sapiens, Similar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AF001954 Homo sapiens growth i
AF078837 Homo sapiens p331NG1
AB031269 Homo sapiens mRNA for
AF187551 Homo sapiens growth i
AF181849 Homo sapiens p471NG1a
AB024402 Homo sapiens mRNA for
AB037387 Homo sapiens ING1 gen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AF062748 Homo sapiens p331RG2
AF149820 Mus musculus p331RG2
AF1757 Mus musculus p331RO1 p1
AF0778835 Homo sapiens p331RO1 p1
AF074076 Homo sapiens p331RO1 p1
AF044076 Homo sapiens candidate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | AB012853 Homo sapiens ING1L mF
| AF053537 Homo sapiens p33 (ING
| AJ006851 Homo sapiens mRNA for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ! AC018191 Drosophila melanoga: ! AC007811 Drosophila melanog
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AC007810 Drosophila melanog
1 AE003719 Drosophila melanog
AF074968 Homo sapiens p47ING3
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       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Joses 1 to 1080)
Nagashima, M., Hagiwara, K., Minter, A.R. and Harris, C.C.
Direct Submission
Submitted (12-Mar) Laboratory of Human Carcinogenesis, National Cancer Institute, 37 Convent Drive Bidg 37 Rm. 2C01, Bethesda, MD 20892, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              68 ATGTTAGGGCAGCAGCAGCAACTGTACTCGTCGGCTGCGCTCCTGAC 117
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Homo sapiens p33 (ING2) mRNA, complete cds.
AF053537
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642 201 692 217

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human. Homo sapiens

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DEFINITION ACCESSION VERSION KEYWORDS

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